

## IL17RLP Nucleotid and Amino Acid Sequence

1	GCACGAGCGATGTCGCTCGTGCCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCC	60
1	<u>M S L V L L S L A A L C R S A V P</u>	17
61	CGAGAGCCGACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAA	120
18	<u>R E P T V Q C G S E T G P S P E W M L Q</u>	37
121	CATGATCTAATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTT	180
38	<u>H D L I P G D L R D L R V E P V T T S V</u>	57
181	GCAACAGGGGACTATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGC	240
58	<u>A T G D Y S I L M N V S W V L R A D A S</u>	77
	<i>Domain I</i>	
241	ATCCGCTTGTTGAAGGCCACCAAGATTGTGTGACGGGCAAAAGCAACTTCCAGTCCTAC	300
78	<u>I R L L K A T K I C V T G K S N F Q S Y</u>	97
	<i>Domain I</i>	
301	AGCTGTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGT	360
98	<u>S C V R C N Y T E A F Q T Q T R P S G G</u>	117
361	AAATGGACATTTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTATTGGG	420
118	<u>K W T F S Y I G F P V E L N T V Y F I G</u>	137
421	GCCCATAAATATTCCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTT	480
138	<u>A H N I P N A N M N E D G P S M S V N F</u>	157
481	ACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGA	540
158	<u>T S P G C L D H I M K Y K K K C V K A G</u>	177
	<i>Domain II</i>	
541	AGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGAATGAGGAGACAGTAGAAGTGAAC	600
178	<u>S L W D P N I T A C K K N E E T V E V N</u>	197
	<i>Domain II</i>	
601	TTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCACTATCATC	660
198	<u>F T T T P L G N R Y M A L I Q H S T I I</u>	217
661	GGGTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATT	720
218	<u>G F S Q V F E P H Q K K Q T R A S V V I</u>	237
	<i>Domain III</i>	

FIG. 1A

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721	CCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGT	780
238	P V T G D S E G A T V Q L T P Y F P T C	257
781	GGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCT	840
258	G S <u>D C I R H K G T V</u> V L C P Q <u>T G V P</u>	277
	Domain IV Domain V	
841	TTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTCTGTGTCT	900
278	<u>F P L</u> D N <b>N</b> K S K P G G W L P L L L L S	297
	Domain V	
901	CTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGG	960
298	L L V A T W V L V A G I Y L M W R H E R	317
961	ATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTT	1020
318	I <b>K</b> K T S F S T T T L <u>L P P I K V L V V</u>	337
	Domain VI	
1021	TACCCATCTGAAATATGTTTCCATCACACAATTGTACTTCACTGAATTTCTTCAAAAC	1080
338	<u>Y</u> P S E I C F H H T I C Y F T E F L Q N	357
	Domain VI	
1081	CATTGCAGAAGTGAGGTCACTCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGT	1140
358	H <u>C R S E V I L</u> E K W Q K K K <u>I A E M G</u>	377
	Domain VII Domain VIII	
1141	CCAGTGCACTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTTCC	1200
378	P V Q W L A <b>T</b> Q K K A A D K V V F L L S	397
1201	AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAG	1260
398	N D V N <b>S</b> V C D G T C G K S E G <b>S</b> P S E	417
1261	AACTCTCAAGACTCTTCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGAT	1320
418	N S Q D S S P C L	426
1321	TCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAA	1380
1381	TGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGA	1440
1441	ACTTCTCCATGTCAAGTAGCAGGTGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGG	1500

FIG. 1B

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**IL17RLP Nucleotide and Amino Acid Sequence**

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1501 CTGCTGCTCCTTGTAGCCCACCCATGAGAAGCAAGWGACCTTAAAGGCTTCCTATCCCAC 1560
1561 CAATTACAGGGAAAAAACGTGTGATGATCCTGAAGCTTACTATGCAGCCTACAAACAGCC 1620
1621 TTAGTAATTAAAACATTTTATACCAATAAAATTTTCAAATATTGCTAACTAATGTAGCAT 1680
1681 TAACTAACGATTGGAAACTACATTTACAACCTCAAAGCTGTTTTATACATAGAAATCAAT 1740
1741 TACAGTTTTAATTGAAAACATAACCATTTTGATAATGCACAATAAAGCATCTTCAGCC 1800
1801 AAAAAAAAAAAAAAAAAA 1816
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**FIG. 1C**

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Percent Similarity: 49.879    Percent Identity: 28.571

$$\begin{array}{c} \text{IL17RLP.aa} \\ \times \\ \text{mIL17R.aa} \end{array}$$
[illegible]

**FIG. 2**

## IL17RLP Protein Analysis

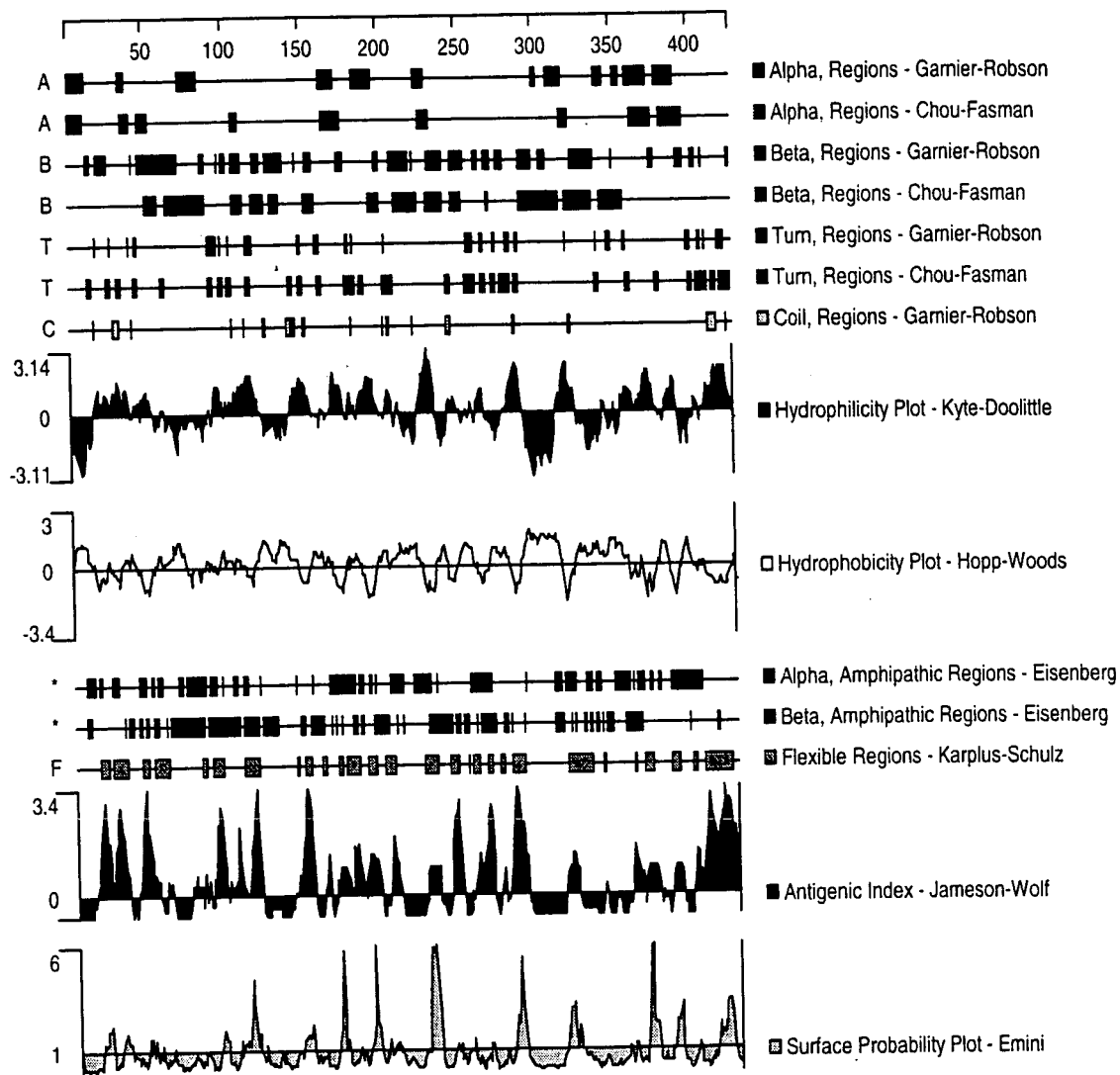


FIG. 3